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QY 5293 AGAAGACCTGCGCCACAGGAGGAATCTAGAGAGGCAATCTGGCTATAGTGGCTTTGC 5314  
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QY 5313 CGAACTGCTGGGCTCCGCTACTT-TAACTGCGAGTGGCTTTGTTTACACTGTGAGG 5255  
Db 514 GTAAACCATCTACTCAAGCTCAGTCAAGCGGAGTGCACCTCTCCACCAAGCTCGAG 573  
QY 5254 GGAACACTGCTTACTGCACTCAGTAAGTGTGAGCTGCTCTCCACCAAGCTCAAG 5195  
Db 574 TGTCCTGCTCAACTCAGA-TGCTGTGATAGCAGTGAAGTTTCAAGTGGATCTT 632  
QY 5194 GATCCCAAGTTGACTTCAGACTGCTGCACTGGCAGTGAGAAATTCAGCCAGTGGAACT 5135  
Db 633 AGCTTGTGCTGGCTCGTGGGGTGGGACCGCTGAACCCAGAC 674  
QY 5134 AGCTTACTGGCTCCATGGGAGTGGGATCCACCGAGCTAGAC 5093  
Db

RESULT 4  
US-08-592-126-114  
Sequence 114 Application US/08592126  
Patent No. 5821091  
GENERAL INFORMATION:  
APPLICANT: Gregory Dolganov  
TITLE OF INVENTION: Transcripts Encoding Immunomodulatory  
TITLE OF INVENTION: Polypeptides  
NUMBER OF SEQUENCES: 151  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dehlinger & Associates  
STREET: 350 Cambridge Avenue, Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/592,126  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Sholtz, Charles K.  
REGISTRATION NUMBER: 38,615  
REFERENCE/DOCKET NUMBER: 4600-0111  
TELEPHONE: (415) 324-0880  
TELEFAX: (415) 324-0960  
INFORMATION FOR SEQ ID NO: 114:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 413 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: H505.seq  
US-08-592-126-114

Query Match 7.8%; Score 135.4; DB 1; Length 413;  
Best Local Similarity 82.0%; Fred. No. 7.9e-32;  
Matches 168; Conservative 0; Mismatches 36; Indels 1; Gaps 1;  
QY 450 TCGGGAGCTGTGGTGGGCTCCACCGAGTTCAAACTCCCGAGCAGCTTTGTTTACACTGT 509  
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QY 510 GAGGTAACCACTACTCAAGCTTCAGCAATGGGGATGCACCTCTCCCAACCAAGCT 569  
Db 269 GAGGGTAACCACTACTCAAGCTTCAGCAATGGGGATGCACCTCTCCCAACCAAGCT 328  
QY 570 CGAGTGTCCCGAGCTCAACCTCAGA-TGCTGTGATAGCAGTGAAGTTTCAACCCAGTGA 628  
Db 329 TGAGTGGCCCGAGCTTACTTCAAGCTGTGCTGCGCAGCAAGAAATTTCAACCAAGTGA 388  
QY 629 TCTAGCTTCTGGCTCGTGGG 653  
Db 389 TCTAGCTTCTGGCTTCTTGGG 413

RESULT 5  
US-09-168-595-114  
Sequence 114 Application US/09168595  
Patent No. 655666  
GENERAL INFORMATION:  
APPLICANT: Gregory Dolganov  
TITLE OF INVENTION: Transcripts Encoding Immunomodulatory  
TITLE OF INVENTION: Polypeptides  
NUMBER OF SEQUENCES: 151  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dehlinger & Associates  
STREET: 350 Cambridge Avenue, Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/168,595  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/592,126  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Sholtz, Charles K.  
REGISTRATION NUMBER: 38,615  
REFERENCE/DOCKET NUMBER: 4600-0111  
TELEPHONE: (415) 324-0880  
TELEFAX: (415) 324-0960  
INFORMATION FOR SEQ ID NO: 114:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 413 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: H505.seq  
US-09-168-595-114

Query Match 7.8%; Score 135.4; DB 4; Length 413;  
Best Local Similarity 82.0%; Fred. No. 7.9e-32;  
Matches 168; Conservative 0; Mismatches 36; Indels 1; Gaps 1;  
QY 450 TCGGGAGCTGTGGTGGGCTCCACCGAGTTCAAACTCCCGAGCAGCTTTGTTTACACTGT 509  
Db 209 TTGCTGAGCTGGGTGAGCTTCCCGAGTTCCAGCTTCTCTGTCGCAATTGTATACACTGT 268  
QY 510 GAGGTAACCACTACTCAAGCTTCAGCAATGGGGATGCACCTCTCCCAACCAAGCT 569  
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/tissue\_type="Purified pancreatic islet"  
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 /clone\_lib="HR85 islet"  
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 Size-selected on agarose gel. Average insert size ~1kb. 5'  
 Xho1 site was destroyed after directional cloning.  
 Amplified once. Contact information: Hiroshi Inoue, MD,  
 Metabolism Div. (Alan Permutt Lab), Washington University  
 School of Medicine, Box 8127, 660 South Euclid Ave., St.  
 Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:  
 314-362-1916, Fax: 314-747-2692."  
 148 a 175 c 175 a 125 t  
 BASE COUNT

Query Match	13.2%; Score 229.8; DB 13; Length 622;
Best Local Similarity	84.9%; Pred. No. 2.6e-37;
Matches 269; Conservative 0; Mismatches 47; Indels 1; Gaps 1;	
QY	146 GGAGGCTCGGGAACAACAAGATTGCTCGCTGTCTCTACCTTGGGAGCTTTGTCGCCAGA 205
DB	620 GGAGGCTCGACACGACAAAGATTGCTCGCTGTCTCTTCCCTCGGAGGCTTTGTCGCCAGA 561
QY	206 AGGGCACCCGCGAGATGCCGGCGACAGCTCTCTGTATCTGTGTGTCTGTAGGCCCCCTACT 265
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QY	266 GTGAGGTGTCTCCAGTCTGTGATACCGGGGGGATCAGGACCCACTTTGAGGAGGCGAGTCT 325
DB	500 GGGAGGTGTCTCC-CAGTCAAGAGGCAATGAGGTTCAGGAACCCACTTCAGGAGGCGAGTCT 442
QY	326 GPCCGTGTATCAGAGCTCGAATGCTGCGGGGAGATTCGTGCTCTCTTACAGAGCTGCA 385
DB	441 GTCCCTTAGCAGAGCTCAATGTCTGCTGGGAGATCTGCTGCTCTCTTCATCAGAGTGGCA 382
QY	386 GGCAGGGACGTTTAAGTCTGCTGAGCTGTGTCCTGCAGCGGCCCTTCCCCACAGTGTCT 445
DB	381 GGCAGGAACGTTTAATCTGCTTAAGTGTGCCACAGCGGCCCTTCCCCACAGTGTCT 322
QY	446 TGTCTCGGGGAGCTGTG 461
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RESULT 13	CD516587	790 bp	mRNA	linear	EST 06-JUN-2003
LOCUS	AGENCOURT 14365752	NIH MGC 181	Homo sapiens	cdna clone	
DEFINITION	IMAGE:30408298.5',	mRNA sequence.			
ACCESSION	CD516587				
VERSION	CD516587.1	BT:31448305			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
	1. (bases 1 to 790)				
REFERENCE	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .				
AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC)				
TITLE	Unpublished				
COMMENT	Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892 Email: <a href="mailto:cgapbs-r@mail.nih.gov">cgapbs-r@mail.nih.gov</a> Tissue Procurement: Dr. Michael Brownstein cdna Library Preparation: Invitrogen Corp cdna Library Arrayed by: The I.M.A.G.E. Consortium [LLNL] DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: NDAM491 row: a column: 11				

High quality sequence stop: 702.  
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/mol\_type="mrna"  
/db\_xref="taxon:9606"  
/clone="IMAGE:30408298"  
/tissue\_type="White Matter"  
/dev\_stage="Unknown"  
/lab\_host="DH10B-Ton A ( T1 and T5 phage resistances) "  
/clone\_lib="NIH MGC 181"  
/note="Vector: pCMV-SPOrt6.1; Site.1: NotI; Site.2: EcoRV (destroyed); Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.42 kb. Library was constructed by (Invitrogen) . Note: this is a NIH\_MGC Library."  
BASE COUNT 160 a 216 c 221 g  
ORIGIN

Query Match 13.2%; Score 229.2; DB 14; Length 790;  
Best Local Similarity 67.2%; Pred. No. 3/5e-37;  
Matches 430; Conservative 0; Mismatches 98; Indels 112; Gaps 3;

QY 145 CGGAGCTGAGGAACAACAAGATTCTCTCTTCTCTACCTCTGGAGCTTGTCCTCCAG 204  
Db 76 CAGAGCTGCACACAGCAAGATTGTGCTGTTCTCTCTCTGAAAGCTTCGTCCAG 135

QY 205 AAGGCACCCGCGATGATCGCGGCGAGAGCTCTCTCTATATGTGGTGTCTGTAGCCCTTAC 264  
Db 136 AGGGGCACCTCACAGATGCGATCTGAGAGTGTCTGTATGATGTGTCTGCAGCCCTTAC 195

QY 265 TGTGAGGTGTCTCCAGCTGAGGTACAGCGGGGGTTCAGGACCCACTTCGAGGAGGCAGTC 324  
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QY 325 TGTCTGTATCAGAGTCTGAATGCTGTCTGGAGAAATTCCTGTCTCTTTAGAGCTGTCT 384  
Db 255 TGACCTTTAGCAGAGCTCGAACTCTGTCTGGAGATCTGTCTGTCTTCAGAGCCCTC 314

QY 385 AGCAGAGGCTTTTAAGTCTGTGAAGTGTGTCTCAGCCGCCCTTCCTCCACAGTGTCT 444  
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QY 445 CTGTCTTGGGAGCTGTGTGGGCTTCCA----- 472  
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QY 473 ----- 472

Db 435 CAGAGATGCCCTGCCAGAGAGAGAAATCTAGAGAGTAGTGTGCCACAGTGTCTTG 494

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QY 515 TAAACCATCTACTTAAGCCTCAGCAATGGCGGATGCACTCTCTCCCAACCAAGTTCAGT 574  
Db 555 TAAACATGCTACTTAAGCCTCAGCAATGGTGGACGTCTCTCTCCCTTACCAACTCTAGC 614

QY 575 GTCCCAAGGTCAACCTCAGA-TGCTGTGATAGAGTTCAGAAATTCAGCCAGTGGATCTTA 633  
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QY 634 GCTTGTGGGCTCCGTGGGGGTGGGACCCGCTGAACCCAGA 673

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RESULT 14					
AQ016709/c					
LOCUS	AQ016709	536 bp	DNA	linear	GSS-09-JUN-1998
DEFINITION	CIT-HSP-2301I23.TR CIT-HSP Homo sapiens genomic clone 2301I23, genomic survey sequence.				

ACCESSION A0016709  
VERSION A0016709.1 GI:3195445  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 536)  
ADAMS, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K.,  
Golden, K., Berry, K., Granger, D., Sub, E., Wible, C., Shizuya, H.,  
Simon, M. and Venter, J.C.  
TITLE Use of a random BAC End Sequence Database for Sequence-Ready Map  
Building (1998)  
JOURNAL Unpublished  
COMMENT Other GSSs: CIT-HSP-2301I23.TF  
Contact: Mark Adams  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: madams@tigr.org  
Clones are available from Research Genetics (info@resgen.com). BAC  
end search page:  
http://www.tigr.org/tldb/humgen/bac\_end\_search/bac\_end\_search.html.  
Seq primer: M13 Reverse  
Class: BAC ends.

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HindIII"  
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ORIGIN

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Best Local Similarity 84.0%; Pred. No. 1.6e-36;  
Matches 267; Conservative 0; Mismatches 50; Indels 1; Gaps 1;  
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DB 519 CAGAGGCTGCAGACAGCAAGATTGCTGCTTCCCTGCTGAGCTTTCATCCCAA 460  
QY 205 AAGGACCCCGCCAGATCGCGGCGAGCTCTCTGTATGTGTGTCTGTAGGCCCTTAC 264  
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QY 325 TGTCTGTATCAGAGCTGAAATGCTGTGTGGAGAAATGCTGCTCTCTTTAGAGCTGTC 384  
DB 340 TGTCTCTTAAACAGAGCTTGTGTGTGGAGATCTGCTGCTCTCTTCAGAGCTGTC 281  
QY 385 AGGCAGGAGCTTTAAGTCTGTGAGCTGTGCTGAGCGGCCCTTCCCGACCTGTCT 444  
DB 280 AGGCAGGAGCTTTAAGTCTGTGAGCTGTGCTGAGCGGCCCTTCCCGACCTGTCT 221  
QY 445 CTCTCTCGGGAGCTGTG 462  
DB 220 CTGTCCCGAGGAGATGG 203

RESULT 15  
BX476445/c  
LOCUS BX476445 420 bp mRNA linear EST 12-JUN-2003

DEFINITION DKFZp686D12186.r1.686 (synonym: hicc3) Homo sapiens cDNA clone  
EX476445 DKFZp686D12186.5', mRNA sequence.  
VERSION EX476445.1 GI:31673701  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 420)  
Koehler, K., Beyer, A., Mewes, H.W., Weil, B., Amid, C., Osanger, A.,  
Fobo, G., Han, M. and Wiemann, S.  
EST (Koehler, K., Beyer, A., Mewes, H.W., Weil, B., Amid, C., et al.)  
TITLE Unpublished  
JOURNAL  
COMMENT Contact: Koehler K  
MIPS  
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany  
This is the 5' sequence of the clone insert  
clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
sequenced by BMFZ (Biomedical Research Center at the Heinrich-  
Heine-University, Dueseldorf/Germany) within the cDNA sequencing  
consortium of the German Genome Project. No sl sequence available.  
This clone (DKFZp686D12186) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
Berlin-Charlottenburg, Germany; Email: clone@rzpd.de.

FEATURES  
Location/Qualifiers  
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CDNA-collection"  
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ORIGIN

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Best Local Similarity 82.8%; Pred. No. 2.2e-35;  
Matches 264; Conservative 0; Mismatches 54; Indels 1; Gaps 1;  
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DB 346 CAGAGGCTGCAGACAGCAAGATTGCTGCTTCCCTGCTGAGCTTTCATCCCAA 287  
QY 205 AAGGACCCCGCCAGATCGCGGCGAGCTCTCTGTATGTGTGTCTGTAGGCCCTTAC 264  
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QY 265 TGTGAGGTCTCTCCAGTCTGGGTACACGGGGGGGTGAGGACCCCTTTCAGGAGGAGTC 324  
DB 226 TGAAGGTATCTCC-CAGTCAGGAGGATGGGTGTGAGGAGCCCACTTCAGGAGGAGTC 168  
QY 325 TGTCTGTATCAGAGCTGAAATGCTGTGTGGAGAAATGCTGCTCTCTTTAGAGCTGTC 384  
DB 167 TGTCTCTTAAACAGAGCTTGTGTGTGGAGATCTGCTGCTCTCTTCAGAGCTGTC 108  
QY 385 AGGCAGGAGCTTTAAGTCTGTGAGCTGTGCTGAGCGGCCCTTCCCGACCTGTCT 444  
DB 107 AGGCAGGAGCTTTAAGTCTGTGAGCTGTGCTGAGCGGCCCTTCCCGACCTGTCT 48  
QY 445 CTGTCTCGGGAGCTGTG 463  
DB 47 CTGTCCCGAGGAGATGGG 29

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